

19BI312 ALGORITHMS IN COMPUTATIONAL BIOLOGY

Hours Per Week :

L	T	P	C
3	1	-	4

Total Hours :

L	T	P	WA/RA	SSH/HSB	CS	SA	S	BS
45	15	-	15	45	-	8	2	2



Source: <https://www.fun-mooc.fr/courses/inria/41007/session01/about>

COURSE DESCRIPTION AND OBJECTIVES:

The course aims to familiarize with the computational problems in Biology useful for aligning sequences, phylogeny tree construction, sequencing technologies etc. The overall objective of the course is train the students to improve the understanding of algorithms used in Bioinformatics. To write novel algorithms to improve speed and accuracy in biological problem solving. Apply the theoretical knowledge of biological problems can be solved using computational approaches.

COURSE OUTCOMES:

Upon completion of the course, the student will be able to achieve the following outcomes:

COs	Course Outcomes	POs
1	Understand the details of the algorithms commonly used in bioinformatics.	1,11
2	Identify which type of algorithm is best suited to describe a given biological problem.	2,3
3	Develop bioinformatics prediction algorithms describing a given biological problem.	1,3,4 5,9
4	Implement and develop prediction tools on a detailed level using the following algorithms: Dynamic programming, Sequence clustering, Weight matrices.	2,4, 5,9

SKILLS:

- ✓ *Develop logical thinking to analyze biological problems.*
- ✓ *Integration of computational programme to fetch answers for biosystems.*
- ✓ *Develop robust programming by implementing dynamic programming skills.*
- ✓ *Develop more robust algorithms which can perform their function with minimum run time.*

UNIT - I **L-9**

INTRODUCTION: Algorithms and complexity, Biological algorithms versus computer algorithms, Iterative versus recursive algorithms, Big-O notations and algorithm design techniques.

UNIT - II **L-9**

GREEDY ALGORITHMS: Exhaustive search, Mapping algorithms, Greedy algorithms, Approximation algorithms.

UNIT - III **L-9**

DYNAMIC PROGRAMMING ALGORITHMS: DNA sequence comparison, Global sequence alignment, Scoring alignment, Local sequence alignment, Alignment with gap penalties, Multiple alignment, EM algorithms, Feed forward and feed backward algorithms.

UNIT - IV **L-9**

GENETIC ALGORITHMS: Crossing over, Linkage and mutation, Operators DNA sequencing, Fragment assembly in DNA sequencing, Protein sequencing and identification.

UNIT - V **L-9**

CLUSTERING AND TREES: Gene expression analysis, Evolutionary trees, Character-based tree reconstruction - small and large parsimony problem.

TEXT BOOK:

1. Neil C. Jones and Pavel A. Pevzner, "An Introduction to Bioinformatics Algorithms", The MIT Press, Cambridge, 2004.

REFERENCE BOOKS:

1. Pavel A. Pevzner, "Computational Molecular Biology: An Algorithmic Approach", The MIT Press, Cambridge, 2000.
2. Wing-Kin Sung, "Algorithms in Bioinformatics: A Practical Introduction", CRC Press, Taylor & Francis Group, 2009.